



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/900,380
Source: FWS
Date Processed by STIC: 11/19/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORRED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <i>10/700,380</i>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input checked="" type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input checked="" type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
TIME: 16:41:40

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

```

3 <110> APPLICANT: Timmermans, Eveline
4           C.A.C.
7           van Gemen, Bob
W--> 8 <120> TITLE OF INVENTION: Method for Quantifying a Ratio Between at Least
W--> 9           Two Nucleic Acid Sequences
W--> 10 <130> FILE REFERENCE: 2183-5581.1US
W--> 11 <140> CURRENT APPLICATION NUMBER: To be Assigned
14 <141> CURRENT FILING DATE: 2003-11-03
15 <150> PRIOR APPLICATION NUMBER: 60/425,055
16 <151> PRIOR FILING DATE: 2002-11-08
W--> 17 <160> NUMBER OF SEQ ID: 18
18 <170> SOFTWARE: PatentIn version 3.1

```

ERRORED SEQUENCES

```

W--> 19 <210> SEQ ID NO: 1
20 <211> LENGTH: 48
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial sequence
W--> 23 <220> FEATURE:
24 <223> OTHER INFORMATION: Synthesized sequence, primer MtD p1
25
W--> 26 <400> SEQUENCE: 1
E--> 27 aattctaata cgactcaacta tagggagaag
28 agccgtttag ttgtggta 48
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 25
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial sequence
W--> 33 <220> FEATURE:
34 <223> OTHER INFORMATION: Synthesized sequence, primer MtD p2
35
W--> 36 <400> SEQUENCE: 2
E--> 37 tctccatcta ttgatgaggg tctta
38 25
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 49
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial sequence
W--> 43 <220> FEATURE:
44 <223> OTHER INFORMATION: Synthesized sequence, MtD p1_2
W--> 45 <400> SEQUENCE: 3

```

ppn 1-5

IMPORTANT: Please ensure that file is saved in ASCII text

Sample (per 1.824)

Sequence Ruler

see item 1 on Error Summary Sheet

same errors

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
 TIME: 16:41:40

Input Set : A:\PTO.YF.txt
 Output Set: N:\CRF4\11192003\J700380.raw

E--> 46 aattctaata cgactcacta taggaaagaa → same
 47 cggggctctg ccatcttaa 49
 48 <210> SEQ ID NO: 4
 49 <211> LENGTH: 20
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial sequence
 W--> 52 <220> FEATURE:
 53 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 54 p2_2 → same
 56 <400> SEQUENCE: 4
 E--> 57 gtaatccagg tcggtttcta
 58 20 →
 59 <210> SEQ ID NO: 5
 60 <211> LENGTH: 32
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Artificial sequence
 W--> 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Synthesized sequence, primer MtD
 65 mb_2 →
 W--> 66 <400> SEQUENCE: 5
 E--> 67 ggccccccca caccaccca agaacagggt cc → same
 68 32 →
 69 <210> SEQ ID NO: 6
 70 <211> LENGTH: 49
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Artificial sequence
 W--> 73 <220> FEATURE:
 74 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
 75 p1 →
 W--> 76 <400> SEQUENCE: 6
 E--> 77 aattctaata cgactcacta taggaaagaa →
 78 cccggcatgt ggtgcataa 49
 79 <210> SEQ ID NO: 7
 80 <211> LENGTH: 23
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Artificial sequence
 W--> 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Synthesized sequence, primer SnrpD
 85 p2 →
 W--> 86 <400> SEQUENCE: 7
 E--> 87 ttccttacat ctctcacccg cta
 88 23 →
 89 <210> SEQ ID NO: 8
 90 <211> LENGTH: 20
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial sequence
 W--> 93 <220> FEATURE:
 94 <223> OTHER INFORMATION: Synthesized sequence, primer
 95 SnrpD2 p2 →

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
TIME: 16:41:40

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

```

W--> 96 <400> SEQUENCE: 8
E--> 97 tgccgcattt tctgggtgtt same
98 20
99 <210> SEQ ID NO: 9
100 <211> LENGTH: 34
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial sequence
W--> 103 <220> FEATURE:
104 <223> OTHER INFORMATION: Synthesized sequence, primer
105 SnrnpD mb_2
W--> 106 <400> SEQUENCE: 9
E--> 107 cgcacatgtgt aaccacgcac ttcctcgca tgcc same
108 34
109 <210> SEQ ID NO: 10
110 <211> LENGTH: 34
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial sequence
W--> 113 <220> FEATURE:
114 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
115 mb
W--> 116 <400> SEQUENCE: 10
E--> 117 gctccgaagc ttctgactct tacctccccg gagg same
118 34
119 <210> SEQ ID NO: 11
120 <211> LENGTH: 49
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial sequence
W--> 123 <220> FEATURE:
124 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
125 p1_4
W--> 126 <400> SEQUENCE: 11
E--> 127 aattctaata cgactcaacta tagggagagg same
128 agacacctgc taggtqtaa 49
129 <210> SEQ ID NO: 12
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial sequence
W--> 133 <220> FEATURE:
134 <223> OTHER INFORMATION: Synthesized sequence, primer MtR
135 p2_2
W--> 136 <400> SEQUENCE: 12
E--> 137 ggtccccccg atatggcgtt cc same
138 22
139 <210> SEQ ID NO: 13
140 <211> LENGTH: 49
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial sequence
W--> 143 <220> FEATURE:
144 <223> OTHER INFORMATION: Synthesized sequence, primer Sig

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
TIME: 16:41:40

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

```

145      p1
W--> 146 <400> SEQUENCE: 13
E--> 147 aattctaata cgactcacta tagggagagg   same
148 actgggcct cagcctgca 49
149 <210> SEQ ID NO: 14
150 <211> LENGTH: 21
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial sequence
W--> 153 <220> FEATURE:
154 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
155      p2
W--> 156 <400> SEQUENCE: 14
E--> 157 ctgaggagac aaggaccatc a   same
158 21
159 <210> SEQ ID NO: 15
160 <211> LENGTH: 32
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial sequence
W--> 163 <220> FEATURE:
164 <223> OTHER INFORMATION: Synthesized sequence, primer Sig
165      mb
W--> 166 <400> SEQUENCE: 15
E--> 167 cgtacgaatg acgtgcct gcgaatcgta cg   same
168 32
169 <210> SEQ ID NO: 16
170 <211> LENGTH: 49
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
W--> 173 <220> FEATURE:
174 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
175      p1
W--> 176 <400> SEQUENCE: 16
E--> 177 aattctaata cgactcacta taggaaagag   same
178 ctctctcccttggccct 49
179 <210> SEQ ID NO: 17
180 <211> LENGTH: 24
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial sequence
W--> 183 <220> FEATURE:
184 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
185      p2
W--> 186 <400> SEQUENCE: 17
E--> 187 gcatctctgt tcatgactgt gtga   same
188 24
189 <210> SEQ ID NO: 18
190 <211> LENGTH: 33
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial sequence
W--> 193 <220> FEATURE:

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003
TIME: 16:41:40

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

194 <223> OTHER INFORMATION: Synthesized sequence, primer TIE
195 mb
W--> 196 <400> SEQUENCE: 18
E--> 197 cgtacgctca acgccagcac gcgcctaccgt acg *Mane*
198 33

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003

TIME: 16:41:41

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11192003\J700380.raw

L:8 M:283 W: Missing Blank Line separator, <120> field identifier
L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:283 W: Missing Blank Line separator, <210> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:1
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:2
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:3
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:63 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:5
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:76 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:6
L:83 M:283 W: Missing Blank Line separator, <220> field identifier
L:86 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:7
L:93 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:103 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:9
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:10
L:123 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:127 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:11
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:12
L:143 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:13
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:14
L:163 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/700,380

DATE: 11/19/2003

TIME: 16:41:41

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11192003\J700380.raw

L:166 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:15
L:173 M:283 W: Missing Blank Line separator, <220> field identifier
L:176 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:16
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:17
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:197 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18